

Resource Summary Report

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Fastml

RRID:SCR_016092

Type: Tool

Proper Citation

Fastml (RRID:SCR_016092)

Resource Information

URL: <http://fastml.tau.ac.il/>

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Description: Web application for the reconstruction of ancestral sequences. It computes maximum likelihood ancestral sequence reconstruction based on the phylogenetic relations between homologous sequences.

Synonyms: The FastML Server

Resource Type: web service, data access protocol, web application, software resource

Defining Citation: [PMID:22661579](#)

Keywords: ancestral, amino-acid, sequence, reconstruction, phylogenetic, relation, accurate, bio.tools

Funding: Israel Science Foundation 878/09;
Bioinformatics Center at Tel-Aviv University

Availability: Free, Freely available

Resource Name: Fastml

Resource ID: SCR_016092

Alternate IDs: biotools:fastml, OMICS_08650

Alternate URLs: <https://bio.tools/fastml>, <https://sources.debian.org/src/fastml/>

License: GNU General Public License

Record Creation Time: 20220129T080328+0000

Record Last Update: 20260728T043514+0000

Ratings and Alerts

No rating or validation information has been found for Fastml.

No alerts have been found for Fastml.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 109 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Zhang P, et al. (2026) Resurrection and characterization of ancestral xylose transporters enhance the capability of xylose uptake in the mixed sugar co-fermentation of Recombinant *Saccharomyces cerevisiae*. *Bioresources and bioprocessing*, 13(1), 1.

Zhao L, et al. (2025) Exploring the Stability and Substrate Profile of Transaminase from *Silicibacter pomeroyi* with Ancestral Sequence Reconstruction. *Chembiochem : a European journal of chemical biology*, 26(13), e202500155.

Jin GT, et al. (2025) A de novo Gene Promotes Seed Germination Under Drought Stress in *Arabidopsis*. *Molecular biology and evolution*, 42(1).

Seppely M, et al. (2025) Impact of Phylogenetic Method Choice on Indel Analyses in HIV-1 Subtype B. *Genome biology and evolution*, 17(6).

Lewitus E, et al. (2025) HIV-1 Vif global diversity and possible APOBEC-mediated response since 1980. *Virus evolution*, 11(1), veae108.

Hart NS, et al. (2025) Widespread and Convergent Evolution of Cone Monochromacy in Galeomorph Sharks. *Molecular biology and evolution*, 42(3).

Walker-Hale N, et al. (2025) Multiple transitions to high l-DOPA 4,5-dioxygenase activity reveal molecular pathways to convergent betalain pigmentation in Caryophyllales. *The New phytologist*, 247(1), 341.

Wallmann A, et al. (2025) Structural and evolutionary determinants of Argonaute function. *Nucleic acids research*, 53(18).

Luo T, et al. (2024) Men with a history of commercial heterosexual contact play essential roles in the transmission of HIV-1 CRF55_01B from men who have sex with men to the general population in Guangxi, China. *Frontiers in cellular and infection microbiology*, 14, 1391215.

Lu Z, et al. (2024) Evolution of optimal growth temperature in Asgard archaea inferred from the temperature dependence of GDP binding to EF-1A. *Nature communications*,

15(1), 515.

Vakirlis N, et al. (2024) Ancestral Sequence Reconstruction as a Tool to Detect and Study De Novo Gene Emergence. *Genome biology and evolution*, 16(8).

Delic S, et al. (2024) The Evolutionary Origins and Ancestral Features of Septins. *bioRxiv* : the preprint server for biology.

Lewitus E, et al. (2024) HIV-1 Gag, Pol, and Env diversified with limited adaptation since the 1980s. *mBio*, 15(3), e0174923.

Delic S, et al. (2024) The evolutionary origins and ancestral features of septins. *Frontiers in cell and developmental biology*, 12, 1406966.

Hu G, et al. (2024) Improving the Quality of Wheat Flour Bread by a Thermophilic Xylanase with Ultra Activity and Stability Reconstructed by Ancestral Sequence and Computational-Aided Analysis. *Molecules (Basel, Switzerland)*, 29(8).

Huang CY, et al. (2024) Subfunctionalization of NRC3 altered the genetic structure of the Nicotiana NRC network. *PLoS genetics*, 20(9), e1011402.

Yada T, et al. (2024) A putative scenario of how de novo protein-coding genes originate in the *Saccharomyces cerevisiae* lineage. *BMC genomics*, 25(Suppl 3), 834.

Iglhaut C, et al. (2024) Please Mind the Gap: Indel-Aware Parsimony for Fast and Accurate Ancestral Sequence Reconstruction and Multiple Sequence Alignment Including Long Indels. *Molecular biology and evolution*, 41(7).

Ewerling A, et al. (2023) Neofunctionalization of ciliary BBS proteins to nuclear roles is likely a frequent innovation across eukaryotes. *iScience*, 26(4), 106410.

Wang X, et al. (2023) Purifying selection leads to low protein diversity of the mitochondrial *cyt b* gene in avian malaria parasites. *BMC ecology and evolution*, 23(1), 49.